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Listing first 45 summaries
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     GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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SDHL_YEAST
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ALIGNMENTS

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SEQUENCE OF 1-10 FROM N.A. STRAIN=K12; MEDLINE=89326124; PubMed=2473940;	overlaphing promocers."; J. Biol. Chem. 261:2441-2450(1986). [6]	K12. Transcription from divergent	G.W.;	11952; 1		SECUTENCE OF 439-514 FROM N.A.	Science 257:771-778(1992).		Escherichia coli genome: DNA sequence of	rland V.D., Blattner	~	SEQUENCE FROM N.A.	NUCLEIC ACIDS RES. 15:213/-2155(1987).	erichia coli K-12.";	"The complete nucleotide sequence of the ilvGMEDA operon of	H. G. W. ;	Pereira R., Taillon B.E.	7.74.2.2.7.7.0.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7	SEQUENCE FROM N.A.		Submitted (AUG-1986) to the EMBL/GenBank/DDBJ databases.	E Harms E		Gene 56:185-198(1987).	erichia coli K-12.";	lete nucleotide sequenc	., Fidanza V., Calhoun	במסטים בייף שקים ינכנט	SEQUENCE FROM N.A.		NCBI_TaxID=562;	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae: Recherichia	-	٦,).	Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine	1-NOV-1988 (Rel. 09, Last sequence up	3-AUG-1987 (Rel. 05, Created)	P04968;	LT 1 ECOLI THE PROPERTY CHANDADD. DDT. 614

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EMBL,
PIR; 182731.,
PDB; 1TDJ; 18-No.,
ECO2DBASE; F050.1; 6Th __
& ECO2DBASE; F050.1; 6Th __
& ECO2DBASE; F050.1; 6Th __
ECO2DBASE; F050.1; 1VA.

InterPro; IPR000634; 8/T_dehydrate1.

InterPro; IPR000534; 8/T_dehydrate1.

INTERPRO; IPR0007721; ThrDh_C.

PFam; PF00291; PALP; 1.

PFAm; PF00291; PALP; 1.

INTERPRO; TIGREAMS; TIGRO1124; 11VA 2Cterm; 1.

PROSITE; PS00165; DEHYDRATASE SER THR; 1.

ISOleucine biosynthesis; Lyase; Pyridoxal phosphate;
FOR TIGREAMS; DESTRUCTURE; Complete proteome.
FOR COMPLETE PRODOXAL PHOSPHATE.

A -> R (IN REF. 2).
A -> R (IN REF. 2).
A -> C (IN REF. 2).

TOTAL THE PRODOXAL PROSPERATE.

ON THE PRODOXAL
    EMBL; X04890; CAA28577.1; -.
EMBL; K03503; AAA24014.1; -.
EMBL; M10313; AAA59054.1; -.
EMBL; M11689; AAA24027.1; -.
EMBL; M32253; AAA24024.1; -.
EMBL; M32253; AAA274024.1; -.
EMBL; M87049; AAA67575.1; -.
EMBL; M8000453; AAC77492.1; -.
EMBL; M25497; AAA24015.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  threonine deaminase.";
Structure 6:465-475(1998).
-!- FUNCTION: Catalyzes th
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MEDLINE=98230745; PubMed=9562556;
Gallagher D.T., Gilliland G.L., Xiao G
Chinchilla D., Eisenstein E.;
"Structure and control of pyridoxal ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: Isoleucine biosynthesis; first step.
-!- SUBUNIT: Homotetramer.
-!- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lopes J.M., Lawther R.P., "Physical identification of an distal portion of the ilvGMEDA Gene 76:255-269(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3). COPACTOR: Pyridoxal phosphate. ENZYME REGULATION: ISOLEDICINE ALLOSTERICALLY INHIBITS WHEREAS VALINE ALLOSTERICALLY ACTIVATES THIS ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step reaction. The first step is a dehydration of threonine, followed by rehydration and liberation of ammonia. Deaminates L-threonine, but also L-serine to a lesser extent. CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
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E.;
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(See http://www.isb-sib.ch/announce/
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ELLQQDAHL 180 ELLQQDAHL 180	IKVDA 120 IKVDA 120	OPVHS 60	Gaps 0;	

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RESULT 2
THD1 S.
THD2 
                                                                                                                                                                                                                                                                                                                    SEQUENCE OF
STRAIN=LT2
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01-FEB-1991 (Rel. 17, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
Threonine dehydratase biosynth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=8825870; PubMed=3290055;
Taillon B.E., Little R., Lawther R.P.;
Taillon B.E., Little R., Lawther R.P.;
"Analysis of the functional domains of biosynthetic threonine deaminase by comparison of the amino acid sequences of three wild-type alleles to the amino acid sequence of biodegradative threonine deaminase.";
Gene 63:245-252(1988).
                                                                                                                                           MEDLINE=89326124; PubMed=2473940;
Lopes J.M., Lawther R.P.;
"Physical identification of an internal promoter,
distal portion of the ilvGMEDA operon.";
Gene 76:255-269(1989).
-!- FUNCTION: Catalyzes the formation of alpha-ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=LT2 / SGSC1412 / ATCC 700720;

MEDLINE=21534948; PubMed=11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria;
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LT2.";
                          FUNCTION: Catalyzes the formation of alpha-ketobutyrate threonine in a two-step reaction. The first step is a de of threonine, followed by rehydration and liberation of CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3) COFACTOR: Pyridoxal phosphate.
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wed by rehydration and liberation of ammonia.
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InterPro; IPR00034; 5/T dehydrtse.
InterPro; IPR0005787; Thr dehydrate1.
InterPro; IPR001721; ThrDh_C.
pfam; pF00291; PALD; 1.
pfam; pF00585; Thr dehydrat C; 2.
TIGRPAMS; TIGR01124; ilvA_2Cterm; 1.
pR0SITE; p800165; DEHYDRATASE_SER_THR;
pR0SITE; P800165; DEHYDRATASE_SER_THR;
DR10steric enzyme; Complete proteome.
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PATHWAY: ISOLeucine biosynthesis; first step
SUBUNIT: Homotetramer.
SIMILARITY: BELONGS TO THE SERINE/THREONINE
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InterPro; IPR001721; ThrDh_C.
InterPro; IPR001721; ThrDh_C.
Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr dehydrat_C; 2.
TIGREAMs; TIGR01124; ILVA_2Cterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
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between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
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03 (Rel. 41, Last sequence update)
03 (Rel. 41, Last annotation update)
03 (Rel. 41, Last annotation (EC 4.3.1.19)
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Pred. No. 3.3
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P46493;
01-NOV-1995
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAINARd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Grebm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                      Submitted (SEP-1995) to the SWISS-PROT data bank.

-!- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step reaction. The first step is a dehydratio of threonine, followed by rehydration and liberation of ammonia -!- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).

-!- COPACTOR: Pyridoxal phosphate (By similarity).
-!- PATHWAY: Isoleucine biosynthesis; first step.
-!- SUBUNIT: Homotetramer (By similarity).
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Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
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28-FEB-2003 (Rel.
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DT 01-OCT-1996 (
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TIGRPAMS; TIGRO1124; ilvA 2Cterm; 1.
PROSITE; PS00165; DEHYDRATASE SER THR; 1.
Isoleucine biosynthesis; Lyase; Pyridoxal
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InterPro; IPR005797; Thr_dehydrateI
InterPro; IPR001721; ThrDh_C.
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BINDING 63
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56662 MW;
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step reaction. The first step is a dehydration of threonine, followed by rehydration and liberation of ammonia.
---- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
---- COFACTOR: Pyridoxal phosphate.
---- COFACTOR: Pyridoxal phosphate.
---- SUBUNIT: Homotetramer (By similarity).
---- SUBUNIT: Homotetramer (By similarity).
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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EMBL; M36383; AAA34705.1; -.
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PIR; S50589; DWBYT.
HSSP; P04966; ITDJ.
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InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR001926; B7_dehydrateI.
InterPro; IPR005787; Thr_dehydrateI.
InterPro; IPR001721; ThDDh_C.
Pfam; PF00585; Thr_dehydrat C; 2.
TIGREAMS; TIGR01124; 11vA_2Cterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
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21.-JUL-1986 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Threonine dehydratase, mitochondrial precursor
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Kielland-Brandt M.C.,
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"Nucleotide sequence of the
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Saccharomycetales; Saccharomycetaceae;
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SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY
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          Yeast 14:1017-1025(1998).
-!- CATALYTIC ACTIVITY: L
-!- COFACTOR: Pyridoxal n
                                                                        transformation marker.
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RESULT 7
THDH_ARXA
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Best Local S
Matches 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
CONFLICT
SEQUENCE
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TRANSIT
CHAIN
                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Dipodascaceae; mitronocina; NCBI Tartn-7777
                                                                                                                                                                                                                                                                    ARXAD
MEDLINE=98398049; PubMed=9730281; Wartmann T., Roesel H., Kunze I., "AILV1 gene from the yeast Arxula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isoleucine biosynthesis; Lyase; Mitochondrion;
                                                          SEQUENCE
                                                                                      NCBI_TaxID=37620;
                                             STRAIN=LS3
                                                                                                                                                                (Threonine deaminase).
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247; Conser
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                                                            FROM
                                                                                                                                                                                                                                                                                                                        LAGISVPPRENLTFQKFLEDLGYTYHDETDNTVYQKFL
                                                                                                                                                                                                                                                                                                                                              LAAFEXGDHEP-DFETRLNELGYDCHDETNNPAFRFFL
                                                                                                                                                                                                                                                                                                                                                                                                   AH-----ILSGANVNFHGLRYVSERCELGEQREALLAVTIPEEKGSFLKFCQLLGGRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRLCQEYLDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKYIA-LHNIRGERL
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. 37, Last sequence up
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atase, mitochondrial p
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Pred. No. 1.4e.
9; Mismatches
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PYRIDOXAL PHOSPHATE.

I -> T (IN REF. 1).
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0801BCBD7EEDDC1F CRC64;
    Bode R., Kunze
adeninivorans
                                                                                                                                                                                           on update)
                                                                                                                                                                             precursor
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                  Kunze
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                                                                                                        Dipodascaceae; Arxula.
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Е
    EG.
                                                                                                                       Saccharomycetes;
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L-threonine phosphate.

2-oxobutanoate

NH (3)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: Isoleucine biosynthesis; first step.
SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Mitochondrial.
SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                   450
                                                                                                     390
                                                                                                                            361
                                                                                                                                                     330
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236; Conserv
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                                                                                                                                                                                                                                                                            GGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRI
                                                                                                                                                                                                                                                                                                                             LHGANFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQ-DAH-LDRVFVPV
                                                                                                                                                                                                                                                                                                                                                                                                          PDGTPDYLKLILTSKVYDVCNETPVTPAVNLSSKLGANIFLKREDLQPVFSFKLRGAYNM
                                                                       AKLHVRYMVGGRPSHPL-QERLYSFEFPESPGAXLRFLNTLGTYWNISLFHYRSHGTDYG
                                                                                                                           GRSVTEFNYRFADAK-----NACIFVGVRLSRGLEERKEILQMLNDGGYSVVDLSDDEM
                                                                                                                                                                                                      GEETFRLCQQVVDEIVLVSTDEICAAIKDVFTETRSIVEPAGALSVAGLVKYVESH----
                                                                                                                                                                                                                   GDETFRLCQEYLDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKYIALHNIRG
                                                                                                                                                                                                                                                       GGGGLIAGVGAYIKRIAPQVKIIGVETYDANAMRQSLQKGERITLSEVGLFADGAAVKIL
                                                                                                                                                                                                                                                                                                         LHGNDFDAAKAECNRLSEKHGLTNIPLFDNPYVIAGQGTIGVELLRQIDVESLKAIFVCI
                                                                                                                                                                                                                                                                                                                                                            MAHL POETRWKGVI ACSAGNHAOGVAYSAKHLNI PATI VMPVVTPAI KYKNVDRLGAKVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PEGA-EYLRAVLRAPVYEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAM
KVLAGISVPSHESDQFQQFLDNLEYPYAEETDNVVYKLFSQG
                                                                                                    PRAVTEFSYRYSNGELEKSDGKAHVYISFSVDNAKAEVPRILDDFKGAGFDAIDISHNEF
                                                                                                                                                    PEIDHSASGYTAILSGANMDFDRLRFVSERAKLGEGSEVFIVATIPEKPGSFGKLIDLVH
                          RVLAAFEXGDHEPD-FETRLNELGYDCHDETNNPAFRFFLAG
                                                PKSHPRYLVGA--NQPVTNERVFRFEFPERPGALVKFLHGVKSKWNITLFHYRNQGSDIA
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550 1
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Pred. No. 1.9e-69;
8; Mismatches 164
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THREONINE DEHYDRATASE.
PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D08CE5BD55CC8A6F
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RESULT 8
THD1_ARATH

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RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottler P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottler P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincher R., Kranz H., Vess H., Holland R., Brandt P., Nyakatura G.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Ronear P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
Coke R., Laudie M., Bezger-Llauro C., Purnelle B., Masuy D.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Pujii C.Y., Shea T.P.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Pujii C.Y., Shea T.P.,
RA Rooney T., Rizzo M., Walts R., Wu D., Peterson J., Van Aken S.,
RA Praser C.M., Xaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Mycras S., Nakazaki N., Shippo S., Takeuchi C., Wada T.,
Fhaliana "., Wanada M., Yasuda M., Tabata S.,
Frasi P., Wanada T., Yamada M., Yasuda M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia; Mourad G., Emerick R., Marion A., Smith A.; Mourad G., Emerick R., Marion A., Smith A.; "Cloning and sequencing of a cDNA encoding threonine dehydratase/deaminase of Arabidopsis thaliana."; (In) Plant Gene Register PGR98-199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ZSG6; Q9SPF1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Threonine dehydratase biosynthetic, chloroplast (EC 4.3.1.19) (Threonine deaminase) (TD).
OMRI OR ATGG10050 OR T2ZK18.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mourad G.S., Smith A.M.;

"Molecular characterization of the promoter sequences, of threonine de Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              feedback insensitive threonine thaliana line GM11b.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20144028; PubMed=10677454; Mourad G., Emerick R., Smith A:; "Molecular cloning and sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (II)
FUNCTION: Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step reaction. The first step is a dehydra of threonine, followed by rehydration and liberation of ammor CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARATH
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InterPro; IPR000634; S/T dehydrtse.
InterPro; IPR0005787; Thr_dehydrateI.
InterPro; IPR001721; ThrDh_C.
InterPro; IPR001721; ThrDh_C.
Pfam; PP00291; PALP; 1.
Pfam; PF00291; PALP; 1.
Pfam; PF00588; Thr dehydrat C; 2.
Pfam; PF00188; Thr dehydrat C; 2.
TIGREAMS; TIGR01124; ilva 2Cterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
INCLUDIATE DESIGNATION OF THE PROSITE PS00165; DEHYDRATASE_SER_THR; 1.
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EMBL; AF221984; AAF32370.1; -.
EMBL; AF177212; AAD54324.1; -.
EMBL; AC010927; AAF04418.1; -.
PIR; T51712; T51712.
HSSP; P04968; 1TDJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING
VARIANT
VARIANT
SEQUENCE
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ENZYME REGULATION: Allosterically inhibited by isoleucine. Stra

GM11b is isoleucine feedback insensitive and is resistant to the

antimetabolite L-O-methylthreonine.

PATHMAY: Isoleucine biosynthesis; first step.

SUBCELIULAR IOCATION: Chloroplast (By similarity).

SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
   451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226;
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VAITSGANMNFDKLRIVTELANVGRQQEAVLATLMPEKPGSFKQFCELVGPMNISEFKYR
                                                                                                                                                                                      AHILSGANVNFHGLRYVSERCELGEQREALLAVTIPEEKGSFLKFCQLLGGRSVTEFNYR
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                                                                                                                                                                                                                                                                                                                                                         TERLCQEYLDDIITVDSDAICAAMKDLEEDVRAVAEPSGALALAGMKKYIALHNIRGERL
                                                                                                                                                                                                                                                                                                                                                                                                                                       GLIAGIAAYVKRVSPEVKIIGVEPADANAMALSLHHGERVILDQVGGFADGVAVKEVGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDSYDQAQAHAKIRAEEEGLTFIPPFDHPDVIAGQGTVGMEITRQAKGPLHAIFVPVGGG
                                                                      FADAKNACIF---VGVRLS----RGLEERKEILQMLNDGGYSVVDLSDDEMAKLHVRYMVGG
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D1; Mismatches
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R -> H (IN STRAIN GM11B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHLOROPLAST (POTENTIAL)
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.3e-66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
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"Biosynthetic threonine deaminase gene of tomato: isolation,
structure, and upregulation in floral organs.";
Proc. Natl. Acad. Sci. U.S.A. 88:2678-2682(1991).
-I- CARALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
-I- COFACTOR: Pyridoxal phosphate.
-I- ENGYME REGULATION: ALLOSTERICALLY INHIBITED BY ISOLEUCINE.
-I- PATHWAY: Isoleucine biosynthesis; first step.
-I- SIBRINTT. Homotetramor.
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P25306;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Threonine debydratease biosynthetic, chloroplast
(EC 4.3.1.19) (Threonine deaminase) (TD)
                                                       CHAIN
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eu Asteridae; lamiids; Solanales; Solanaceae; Solanum.
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Pfam; PF00585; Thr_dehydrat_C; 2.
Pfam; PF00585; Thr_dehydrat_C; 2.
TIGREAM8; TIGR01124; 11vA 2Cterm; 1.
TIGREAM8; TIGR01124; 11vA 2Cterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER THR; 1.
PROSITE; PS00165; DEHYDRATASE_Chloroplast; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                    EMBL; M61914; AAA34171.1; -.
EMBL; M61915; AAA68097.1; -.
                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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InterPro; IPR00634; S/T_dehydrtse.
InterPro; IPR005787; Thr_dehydrate1.
InterPro; IPR001721; ThrDh_C.
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                                                                                                  Allosteric enzyme;
TRANSIT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homotetramer.
SUBCELLULAR LOCATION: Chloroplast.
MISCELLANEOUS: EXPRESSION IN MATUR
                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS
                                                                                                                                                                                                                                                          A38628; A38628.
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CHLOROPLAST.
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STRAIN=CV. PUSA 261 / PCITD 2; TISSUE=Seed;
STRAIN=95232188; PubMed=7716234;
MEDLINE=95232188; PubMed=7716234;
John S.J., Srivastava V., Guha-Mukherjee S.
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European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ifled and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
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SUBCELLULAR LOCATION: Chloroplast (Fissue Specificity: Found at Higher
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Isoleucine biosynthesis; Lyase; Chloroplast; Pyridoxal

Allosteric enzyme; Transit peptide.
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                                                                                                     EGVAVKRIGDETFRLCQEYLDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKY
                                                                                                                                                                                                                                                                                                                                   LDRVFVPVGGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFA
                                                                                                                                                                                                                                                                                                                                                                                                 AVRGFGGEVLLHGANFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAH
                                                                                                                                                                                                                                                                                                                                                                                                                                              KLRGAYAMMAGITEEQKAHGVITASAGNHAQGV--AFSSARLGVKALIVMPTATADIKVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADSQPLSGAPEGAEYLRAVLRAPVYEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSF
                                                                                                                                                           HGSLSFTEITYRFTSHRRSILVLMLKLEPWRYIE---KMIEMMKYSGVTVLNISHNELAV
                                                                                                                                                                                                                                                                                                                                                                        GVRALGADVVLWGHTFDEAKTHAVELCEKDGLRTIPPFEDPAVIKGQGTIGSEINRQIKR
                                                                                                                                                                                                                                                                                                                                                                                                                             KLRGPYNMMSSLSHEEIDKGVITASAGNHAQGVPFPFPGRRLKCVAKIVMPTTTPNIKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSDEL-----PEYLRDVLRSPVYDVVVESPVELTERLSDRLGVNFYVKREDRQRVFSF
                                                                           VLAAFEXGDHEPDF-----ETRLNELGYDCHDETNNPAF 508
                                                                                                                                LHVRYMVGGRPSHPLQERLY-SFEFPESPGAXL-RFLNTLGTYWNISLFHYRSHGTDYGR
                                                                                                                                                                                   -GGRSVTEFNYRFADAKNACIFVGVRLS--RGLEERKEILQMLNDGGYSVVDLSDDEMAK
                                                                                                                                                                                                              CEMYRIKNDNMVGIVSGANMNFRKLHKVSELAVLGSGHEALLGTYMPGQKGCFKTMAGLV
                                                                                                                                                                                                                                                                  DGATVAVIGEYTFARCODVVDAMVLVANDGIGAAIKDVFDEGRNIVETSGAAGIAGM--Y
                                                                                                                                                                                                                                                                                                                       IDAVFVPVGGGGLIAGVÄÄFFKQIÄPQTKIIVVEPYDÄÄSMALSVHÄEHRÄKLSNVDTFÄ
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ilarity 41.5%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 P
65153 MW;
                                                    -FLCEIVIRKNQIDDLGYPYEIDQYNDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 937.5; DB 1
Pred. No. 5.4e-56;
2; Mismatches 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THREONINE DEHYDRATASE BIOSYNTHETIC. PYRIDOXAL PHOSPHATE (BY SIMILARITY); 01D7736AC92BCDEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHLOROPLAST (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178;
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Best Local Sir
Matches 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 result of mechanical wounding.";
Plant Cell 4:1157-1170(1992).
-i- CATALYTIC ACTIVITY: L-threonine =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hildmann T., Ebneth M., Pena-Cortes H., Sanchez-Serrano J.J., Willmitzer L., Prat S., "General roles of abscisic and jasmonic acids in gene activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 2.
PROSITE; PS00165; DEHYDRATASE_SER_THR; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allosteric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001926; B6_enzyme_beta
InterPro; IPR000634; S/T_dehydrtse
InterPro; IPR001721; ThrDh_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X67846; CAA48039.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Desiree; TISSUE=Leaf; MEDLINE=93005746; PubMed=1392612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COPACTOR: PYTICATAL Phosphate.

COPACTOR: PYTICATION: ALLOSTERICALLY INHIBITED BY ISOLEUCINE.

PATHMAY: Isoleucine biosynthesis; first step.

SUBUNIT: Homotetramer.

SUBCELLULAR LOCATION: Chloroplast.

TISSUE SPECIFICITY: FLORAL HUDS OF UNTREATED PLANTS. AFTER ABA TREATMENT OR MECHANICAL WOUNDING IS MOSTLY ACCUMULATED IN LEAVI
TO A LESSER EXTENT IN STEMS, BUT NOT IN ROOTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDUCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQ0468; PQ0468.
; P04968; 1TDJ.
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                             454
                                                                              240
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                                                                                                                                                                                                                                     336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 PFDHPMVIAGQGTLALELLQQDAHLDRVFVPVGGGGLAAGVAVLIKQLMPQIKVIAVEAE
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LGTYWNISLFHYRSHGTDYGRVLAAFEXGDHEPD-FETRLNELGYDCHDETINNPAFRFFFL
                                                                                                                                                                                    DNEALLATFMI
                                                                                                                                                                                                                                     QREALLAVTIPEEKGSFLKFCQLLGGRSVTEFNYRF-ADAKNACIFVGVRLSRGLEERKE
                                                                                                                                                                                                                                                                                                                                              DLFEDVRAVAEPSGALALAGMKKYIALHNIRGERLAHILSGANVNFHGLRYVSERCELGE
                                                                                                                                                                                                                                                                                                                                                                                               GAASMTLSLYEGHRVKLENVDTFADGVAVALVGEYTFAKCQELIDGMVLVRNDGISAAIK
                                                                                MIKKLNSSNMKTFNFSHNELVAEHIKHLVGGSAS--ISDEIFGEFIFPEKAGTLSTFLEA
                                                                                                                                 ILQMLNDGGYSVVDLSDDEMAKLHVRYMVGGRPSHPLQERLY-SFEFPESPGAXLRFLNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biosynthesis; Lyase; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                    EQPGSFKTFAKLVGSMNITEVTYRFTSERKEALVLYRVDVDE-KSDLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABA), JASMONIC ACID (JA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 642; DB 1;
No. 2.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2-oxobutanoate +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                          RA Kunst F. (Ogasawaza N., Moszer I., Albertini A.M., Alloni G., Ra Borriss R., Bourster L., Brans A., Braun M., Brignell S.C., Bron S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Para B., Brouillet S., Errington J., Fabret C., Ferrari E., Foulger D., Daniel R.A., Prans K.D., Errington J., Fabret C., Ferrari E., Foulger D., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Ra Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Ra Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., RA Ghim S.Y., Glaser P., Koffeau A., Golightly E.J., Grandi G., RA Ghiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Albert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Albert J., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Medina K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudeya B., Park S.H., RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudeya B., Park S.H., RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sadaie Y., Mambutt R., Wedler E., Wedler E., Scoffone F., Soldo B., Rakeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A., Tacconi E., Takagi T., Takahashi H., Takamaru K., Vanamoto H., Yanane K., Yasawnoto K., Yata K., Yasawoto K., Yata K., Yasawoto K., Yata K., Yasawoto K., Yata K., Yashi S., Yanamoto H., Yanane K., Yasawoto K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., Tanbria R., Wedler E., Wedler H., Weitzenegger T., Subtilus R., Subtilus R., Forta R., Weitzenegger T., Subtilus R., Subtilus R., Weitzenegger T., Subtilus R., Subtilus R., Subtilus R., Subti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THD1_BACSU
P37946;
01-OCT-1994
                                                                                Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the Bacillus subtilis the serA and kdg loci cloned in a yeast artimicrobiology 142:2005-2016(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98044033; PubMed=9384377;
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28-FEB-2003 (Rel.
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  FUNCTION: Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step reaction. The first step is a dehydration of threonine, followed by rehydration and liberation of ammonia CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298
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30, Last seq
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biosynthetic (EC 4.3.1.19)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zumstein E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillaceae; Bacillus
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artificial chromosome.";
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Best Local Similarity
Matches 149; Conser
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EMBL; L77246; AAA96639.1; -.
EMBL; Z99115; CAB14095.1; -.
PIR; A69644; A69644.
HSSP; P04968; 1TDJ.
SubtiList; BG10673; i1vA.
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR001634; S/T_dehydrtse.
InterPro; IPR001631; ThrDh_C.
InterPro; IPR001721; ThrDh_C.
        THD1 BACHD STANDARI OPKC63; 09KC63; 28-FEB-2003 (Rel. 41, I 28-FEB-2003 (Rel. 41, I 28-FEB-2003 (Rel. 41, I Threconine dehydratase h
                                                                                                            BACHD
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Pfam; PF00585; Thr dehydrat C; 1.
PROSITE; PS00165; DEHYDRATASE SER THR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR: Pyridoxal phosphate.
PATHWAY: Isoleucine biosynthesis; first step.
SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                       DAICAAMKDLFEDVRAVAEPSGALALAGMKKYIALHNIRGERLAHILSGANVNFHGLRYV 327
                                                                                                                                                                                                                                                                                                                                                                                                      KVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFRLCQEYLDDIITVDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGFTWVPPFDHPMVIAGQGTLALELLQQ-DAHLDRVFVPVGGGGLAAGVAVLIKQLMPQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGVAFSSARLGVKALIVMPTATADIKVDAVRGFGG---EVLLHGANFDEAKAKAIELSQQ 148
                                                                                                                                                                         L-ONKADYGPLIERMNKKPFHYVEVNKDE
                                                                                                                                                                                                          LSRGLEERKEILQMLNDGGYSVVDLSDDE 413
                                                                                                                                                                                                                                                                                                         GKVCTSILELYNECAVVAEPAGALSVAALDLY--KDQIKGKNVVCVVSGGNNDIGRMQEM
                                                                                                                                                                                                                                                                                                                                                                                                                                        ESRTFIHPFDDPDVMAGOGTLAVEILNDIDTEPHFLFASVGGGGLLSGVGTYLKNVSPDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGVAFSCKHLGIHGKIFMPSTTPRQKVSQVELFGKGFIDIILTGDTFDDVYKSAAECCEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPLQRNDRLSERYECNIYLKREDLQVVRSFKLRGAYHKMKQLSSEQTENGVVCASAGNHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMAGLTEEQKAHGVITASAGNHA
                                                                                                                                                                                                                                      KERSLIFEGLOHYFIVNFPORAGALREFLDEVLGPNDDITRFEYTKKNNKSNGPALVGIE
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422
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                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.4%; Score 642; DB 1; 38.3%; Pred. No. 3.2e-36; tive 74; Mismatches 156
     Created)

Last sequence update)

Last annotation update)

biosynthetic (EC 4.3.1.19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRIDOXAL PHOSPHATE (BY SIMILARITY).

H -> D (IN REF. 2).

V -> A (IN REF. 2).

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                                                                                           PRT;
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Best Local :
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Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
InterPro; IPR001721; ThTDh_C.
Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
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HSSP; P04968; 1TDJ.
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385
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                                                                                                                                                                                                                                                                                                                                                                                    HKMTFIHPPDQEKIVÄGQGTVGMEIMNDIDDNIDYLFCSIGGGGLISGVGTYIKSISPRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMAGLTEEQKAHGVITASAGNHA
LSRGLEERKEILQMLNDGGYSVVDLSDDE
                                                      RERSLIYEGLQHYFIIQFPQRAGALKEFILDVLGPDDDITRFEYTKKNNKSNGPVLIGIE
                                                                                                       SERCELGEOREALLAVTIPEEKGSFLKF-COLLG-GRSVTEFNYRFADAK-NACIFVGVR 384
                                                                                                                                                             GKICTTILNLYNQDAIVAEPAGAMPIAALDFF--KDEIKGKTVVCVLSGGNNDIGRMQEM
                                                                                                                                                                                               DAICAAMKDLFEDVRAVAEPSGALALAGMKKYIALHNIRGERLAHILSGANVNFHGLRYV 327
                                                                                                                                                                                                                                                                       KVIGCEPAGAPAMKESLKQGKVIELEKIDKFVDGAAVKKVGEIPFEICQKILEDIVLVPE
                                                                                                                                                                                                                                                                                                      KVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFRLCQEYLDDIITVDS
                                                                                                                                                                                                                                                                                                                                                                                                                                    QGFTWVPPFDHPMVIAGQGTLALELLQQ-DAHLDRVFVPVGGGGLAAGVAVLIKQLMPQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGVAFSSARLGVKALIVMPTATADIKVDAVRGFGG---EVLLHGANFDEAKAKAIELSQQ 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPLQKNQVLSERYECNVYLKREDMQVVRSFKIRGAFHQISSIPKEELNNGVVCASAGNHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53
415 AA;
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7; Mismatches
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Pred. No. 6.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRIDOXAL PHOSPHATE (BY SIMILARITY).
; BF49D28E65C7CFA2 CRC64;
  413
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., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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Delorme C.,
Renault P.;
Submitted (N
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01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Threonine dehydratase biosynthetic (EC 4.3.
                         CONFLICT
CONFLICT
                                                                              InterPro; IPROU1/21, 4...---
Pfam; PPO0291; PALP; 1.
Pfam; PP00285; Thr dehydrat C; 1.
Pfam; PP00585; Thr dehydrat C; 1.
PROSITE; PS00165; DEHYDRATASE SER THR; 1.
PROSITE; PS00165; Dyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21235186; PubMed=11337471; Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-NCDO 2118;
MEDLINE-93015710; PubMed=1400210;
Godon J.-J., Chopin M.-C., Ehrlich S.D.;
"Branched-chain amino acid biosynthesis;
subsp. lactis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deaminase).
ILVA OR LL1227.
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                                                                                                                                                                     InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis (subsp. lactis) (Streptococcus lactis). Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; L
                                                                                                                                                                                                  PIR; C86778; C86778.
HSSP; P04968; 1TDJ.
            SEQUENCE
                                                                                                                                                                                                                                EMBL; AE006354; AAK05325.1; -.
                                                                                                                                                                                                                                          EMBL; U92974; AAB81922.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol.
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                                                                                                                                                      ; IPR001926; ; IPR000634; ; IPR001721;
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393
            45577
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S/T_dehydrtse.
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            WW.
                         PYRIDOXAL PHOSPHATE (BY A -> S (IN REF. 1).
D -> N (IN REF. 1).
H -> R (IN REF. 1).
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            AFDAC61464D7E977
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(EC 4.3.1.19)
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AC Q10766;
DT 01-0CT-1996 (Rel. 34
DT 01-0CT-1996 (Rel. 34
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DE Probable threonine d
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Best Local
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Bagham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                   Fleischmann R.D., Alland D., Eisen
Peterson J., DeBoy R., Dodson R., G
Kolonay J.F., Nelson W.C., Umayam L
Delcher A., Utterback T., Weidman J
                                                                                    SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D.,
                                                                                                                                                                                                                                                                                                                                                                   Corynebacterineae;
NCBI_TaxID=1773;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                             Bishai W.;
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laboratory sti
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nilarity 37.4%;
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. 41, Last anno
ne deḥydratase |
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             of.
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               Mycobacterium tuberculosis clinical
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Pred. No. 2.2e-33;
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L.A., Ermolaeva
J., Khouri H.,
                                                                                        J.A.,
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M.L., Haft
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                                            ⁄а М.D., Sa
Gill J.,
                                            r L., White O.,
t D., Hickey E.,
M.D., Salzberg S
Gill J., Mikula P
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                    and
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                                                            S.L.,
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Query Match
Best Local Similarity
Matches 170; Conserv
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DOMAIN
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InterPro; IPR001926; B6 enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
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EMBL; AE007027; AAK45877.1;
PIR; D70763; D70763.
HSSP; P04968; ITDJ.
TIGR; MT1610; --
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Pfam; PF00585; Thr_dehydrat_C; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; DB 1; Length 429; 6.4e-32;
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Db 385 ETGEALVGIELGS-AADLDGLLARWRATDIHVEALEPGSPAYRYLL 429

Search completed: December 18, 2003, 15:28:48
Job time: 18 secs

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	December 18,	OM protein - protein search, using sw model		Copyright	
(without alignments) 2353.843 Million cell updates/se	December 18, 2003, 15:27:16 ; Search time 21 Seconds	using sw model		Copyright (c) 1993 - 2003 Compugen Ltd.	Concern sound on E 1 E
s) ell updates/se	Seconds				

Title:	NP418220
Perfect score:	2633
Sequence:	1 MADSQPLSGAPEGA

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.....LGYDCHDETNNPAFRFFLAG 514

cell updates/sec

Scoring table: BLOSUM62DX Gapop 10.0 ,

Gapext 0.5

283308 seqs,

96168682 residues

Searched:

Total number of hits satisfying chosen parameters:

283308

Minimum DB Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution

SUMMARIES

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	L-serine ammonia-1	threonine dehydrat	hypothetical prote	threonine dehydrat	threonine dehydrat	threonine ammonia-	threonine dehydrat	threonine deaminas	threonine dehydrat							

ALIGNMENTS

threonine ammonia-lyase (EC 4.3.1.19), biosynthetic - Escherichia coli (strain N;Alternate names: L-serine dehydratase; serine deaminase; threonine deaminase C;Species: Escherichia coli K-12)

Gene 56, 185-198, 1987
A;Title: The complete nucleotide sequence of the ilvGMEDA cluster of Escherichia coli K-A;Reference number: A91578; MUID:88056322; PMID:3315862
A;Accession: B27310 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jun-2002 C;Accession: B27310; C26287; E26570; S48895; S30670; I41304; G65180 R;Cox, J.L.; Cox, B.J.; Fidanza, V.; Calhoun, D.H.

A; Molecule type: DNA 1;Residues: 1-514 <COX> Cross-references: GB:M32253

A;Experimental source: strain K12 R;Wek, R.C.; Hatfield, G.W.

J. Biol. Chem. 261, 2441-2450, 1986 A,Tille: Nucleotide sequence and in vivo expression of the ilvY and ilvC genes in Escher A,Reference number: A92575; MUID:86111952; PMID:3003115 A,Accession: C26287

A; Molecule type: DNA A; Residues: 439-514 <WEK>

A;Cross-references: GB:K03503
A;Experimental source: strain K12
R;Lawther, R.P.; Wek, R.C.; Lopes, J.M.; Pereira, R.; Taillon, B.E.; Hatfield, G.W. Nucleic Acids Res. 15, 2137-2155, 1987
A;Title: The complete nucleotide sequence of the ilvGMEDA operon of Escherichia coli K-1 A;Reference number: A26570; MUID:87174741; PMID:3550695
A;Accession: E26570

Molecule type: DNA;Residues: 1-242,'G',244-514 <LAW1>;Cross-references: GB:M32253; NID:G146465; PIDN:AAA24024.1; Я. Р.

PID:g146470

submitted to the EMBL Data Library, December 1987

Reference number: S48893 Accession: S48895

Residues: 1-514 <LAW2>

A;Cross-references: EMBL:X04890; NID:g288528; PIDN:CAA28577.1; PID:g288533 R;Daniels, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R. Science 257, 771-78, 1992 A;Title: Analysis of the Escherichia coli genome: DNA sequence of the reginal Reference number: S30660; MUID:92358234; PMID:1379743

of the region from

A; Reference number: A; Accession: S30670

A;Cross-references: EMBL:M87049; NID:g836656; PIDN:AAA67575.1; PID:g148179
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992
R;Lopes, J.M.; Lawther, R.P. A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-121,'X',123-139,'R',141-514 <DAN>

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A;Title: Physical identification of an internal promoter, ilvAp, in the dis A;Reference number: I41304; MUID:89326124; PMID:2473940
A;Recession: I41304
A;Recession: I41304
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: I-10 <RES
A;Cross-references: GB:M25497; NID:g341363; PIDN:AAA24015.1; PID:g538347
A;Cross-references: GB:M25497; NID:g341363; PIDN:AAA24015.1; Burland, V.;
A;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
A,; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G65180
         RESULT 2
B91217
threonine
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-514 <BLAT>
A;Residues: 1-514 <BLAT>
A;Residues: 1-514 <BLAT>
A;Residues: 1-514 <BLAT>
A;Coss-references: GB:AE000453; GB:U00096; NID:g2367276; PIDN:AAC77492.1; PID:g1790
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: ilvA
A;Map position: 85 min
C;Function:
A;Map position: catalyzes the deamination of threonine to yield alpha-ketobutyrate an A;Pathway: isoleucine-valine biosynthesis
A;Note: this is the first enzyme in the isoleucine biosynthetic pathway
C;Superfamily: threonine dehydratese
C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase;
C;Keywords: pyridoxal phosphate (Lys) (covalent) #status predicted
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                                                                                                                                             XGDHEPDFETRLNELGYDCHDETNNPAFRFFLAG
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RESULT 3
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Chroonine ammonia-lyase (EC 4.3.1.19) [similarity] - Escheric C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_chan C;Accession: C86063
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasne iler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E Nature 409, 529-533, 2001
A;Tile: Genome sequence of enterohemorrhagic Escherichia col A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C86063
A;Status: preliminary
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B91217
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-514 <HAY>
A;Residues: 1-514 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB38129.1; PID:g13364181; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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C;Superfamily: threonine dehydratase
C;Keywords: ammonia-lyase; carbon-nitrogen
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C;Date: 18-Uul-2001 #sequence_revisi
C;Accession: B91217
R;Hayashi, T.; Makino, K.; Ohnishi,
gasawara, N.; Yasunaga, T.; Kuhara,
DNA Res. 8, 11-22, 2001
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                                                                                                                     GRSVTEFNYRFADAKNACIFVGVRLSRGLEERKEILQMLNDGGYSVVDLSDDEMAKLHVR
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                       XGDHEPDFETRLNELGYDCHDETNNPAFRFFLAG
                                                          YMVGGRPSHPLQERLYSFEFPESPGALLRFLNTLGTHWNISLFHYRSHGTDYGRVLAAFE
                                                                            YMVGGRPSHPLQERLYSFEFPESPGAXLRFLNTLGTYWNISLFHYRSHGTDYGRVLAAFE
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Pred. No. 7.2e-176;
3; Mismatches 1;
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Glasner, lanta, E.;

J.D.; Rose, Potamousis, 02-Aug-2002

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Apodaca,

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#text_change

Escherichia coli (strain

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threonine ammonia-lyase (EC 4.3.1.19) [similarity] - Salmonella enterica sub C.Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AB0924 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, Cth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, S.; O'Gaora, P.; S.; O'Gaora, P.; Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; A;Althors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; A,Title: Complete genome sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Salmonella er a.Peferone sequence of a multiple drug resistant Sa
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A;Residues: 1.515 <STO>
A;Cross-references: GB:AE005174; NID:g12518630; PIDN:AAG58967.1;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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;Gene: STY3652
;Superfamily: threonine dehydratase
;Keywords: ammonia-lyase; carbon-ni
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                                                                                                                    YMVGGRPSHPLQERLYSFEFPESPGAXLRFLNTLGTYWNISLFHYRSHGTDYGRVLAAFE
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                                             LGDHEPDFETRLHELGYECHDESNNPAFRFFLAG
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Pred. No. 1e-168;
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threonine ammonia-lyase (EC 4.3.1.19), biosynthetic - Salmonella typhimurium N;Alternate names: L-serine dehydratase; serine deaminase; threonine deaminase C;Species: Salmonella typhimurium C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jun-2002 C;Accession: JT0278 Gene 63, 245-252, 1988 A; Title: Analysis of the functional domains 0f biosynthetic threonine deaminase

A; Molecule type: DNA A; Residues: 1-514 <TAI> A; Cross-references: GB: M26670; A; Note: the authors translated C; Genetics: A; Reference number: JT0278; A; Accession: JT0278

nine deaminase

MUID:88255870;

PMID:3290055

γď compa

NID:g341512; PIDN:AAA27150.1; the codon CTG for residue 169

PID:g514966 as Ile

A;Gene: ilvA
A;Map position: 83
C;Function:

min

A; Description: catalyzes the deamination of A; Pathway: isoleucine-valine biosynthesis isoleucine

threonine

ť

yield alpha-ketobutyrate

am

biosynthetic

pathway

hydro-lyase;

A; Note: C; Superf C; Keywor F; 62/Bir Note: this is the first enzyme in the Superfamily: threonine dehydratase lyase;

;Keywords: ammonia-lyase; carbon-nitrogen l; ;62/Binding site: pyridoxal phosphate (Lys) ase; carbon-oxygen (covalent) #status lyase; hyo predicted

Query Match
Best Local Similarity
Matches 483; Conser 94.8%; 4.1e-1 DB 1; 1e-167 Length 0

Conservative 18; Score 2497; I Pred. No. 4.1e 18; Mismatches Indels 0; Gaps

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threonine ammonia-lyase (EC 4.3.1.19) [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis C;Species: Yersinia pestis C;Species: Yersinia pestis C;Pate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 21-Jun-2002 C;Accession: AG0474 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, $53-527, 2001 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; Phill: Holden, M.; Rutherson: AG0474 A;Status: preliminary A;Status: preliminary A;Status: preliminary A;Cross-references: GB:AL590842; PIDN:CAC93363.1; PID:g15981809; GSPDB:GN00175 C;Genetics: 1-514 *KUR- A;Cross-references: GB:AL590842; PIDN:CAC93363.1; PID:g15981809; GSPDB:GN00175 C;Genetics: A;Gene: ilvA C;Superfamily: threonine dehydratase C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase
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                                                                        FKLRGAYAMMAGLTEEQKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDA 120
                                                                                                                    MAVSQPLSAAPCGAEYLRAILRAPVYEVAQVTPLQVMEKISSRVGNTVLVKREDRQPVHS
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                                        FKLRGAYAMISSLTEEQKACGVVTASAGNHAQGVALSAHKMGIKALIVMPVATADIKVDA
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Pred. No. 9.
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ALHNIRGERLAHILSGANVNFHGLRYVSERCELGEQREALLAVTIPEEKGSFLKFCQLLG
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                                                                                                                  QQHNIQGERLAHVLSGANVNFHGLRYVSERCELGEQREALLAVTIPEQKGSFLRFCELLG
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                                        YMVGGRÞSKÞLRERLFSFEFÞESÞGALLKFLHTLGTHWNISLFHYRSHGTDFGRVLAAFE
                                                                             GRSVTEFNYRYADAENACIFVGVRLTRGYAERVEILAELQDKGYQVVDLSDDEMAKLHVR
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A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82374
A;Ketaus: preliminary
A;Molecule type: DNA
A;Residues: 1-510 <HEI>
A;Cross-references: GB:AE004094; GB:AE003852; NID:g9654407; PIDN:AAF93205.1; GSPDB:GA;Cross-references: GB:AE004094; GB:AE0 C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_chang
C;Accession: E82374
C;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin,
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000 RESULT E82374 threonine ammonia-lyase (EC 4.3.1.19) [similarity] - Vibrio cholerae (strain 70.2%; Score 1849.5; DB 2; Pred. No. 8.8e-122; 20-Aug-2000 #text_change 21-Jun-2002 Gwinn, M.L.; Dodson, R.J.; H.; Dragoi, I.; Sellers, P 510; GSPDB:GN001 N16961 Boud sero

Local Similarity

354;

Conservative

64;

Mismatches

81;

Indels Length

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Gaps

13

GAEYLRAVLRAPVYEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMAG

GAEYLRQILRSPVYEVANVTPLQTMPRLSARIGNQVQIKREDRQPVHSFKLRGAYNMVSH

89 73

LTEEQKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRGFGGEVLLHG

188 193

AAGVAVLIKQIMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETF

ANFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHLDRVFVPVGGGGL

192

132 67

127

252

187

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RESULT 8
B83479
threonine dehydratase, biosynthetic PA1326 [imported] - Pseudomonas aeruginc C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Jun-2002 C;Accession: B83479
R;Stover; C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hicladman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lari, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
"Millor Gramlete genome sequence of Pseudomonas aeruginosa PA01, an opport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-515 <STO>
A;Cross-references: GB:AE004562; GB:AE004091;
A;Experimental source: strain PAO1
C;Genetlos:
A;Gene: ilvA2; PA1326
E;Superfamily: threonine dehydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
A; Molecule type: DNA
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GGRSVTEFNYRFADAKNACIFVGVRLSRGLEERKEILQMLNDGGYSVVDLSDDEMAKLHV
                                                                                                                            EGVĀVKRIGDETFRLCQEYLDDIITVDSDĀICAAMKDLFEDVRĀVĀEPSGALĀLĀGMKKY
                                                                                                                                                                   LDAIFVPVGGGSLIAGIAAYVKHLRPDIRVIGVEPEDSNCLQAALAAGERVVLGQVGLFA
                                                                IALHNIRGERLAHILSGANVNFHGLRYVSERCELGEQREALLAVTIPEEKGSFLKFCQLL
                                                                                                                                                                                             LDRVFVPVGGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFA
                                                                                                                                                                                                                               VLARGGEALLHGDAFPDALAHALQLAEREGMTFVPPYDDPDVIAGQGTVAMEILRQHSGR
                                                                                                                                                                                                                                                                                                      FKLRGAYAMMAGLTEBOKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDA 120
                                                                                                                                                                                                                                                                                                                                                  LSASKPLL-----AGYVESILAAPVYDVAVETPLQVAPQLSQRLGNRVLLKREDLQPVFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLCQBYLDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKYIALHNIRGERLAH
                                               VARERTEGOTLVAIDSGANINFDRLRHVAERAELGEOREAIIAVTVAERPGSFKAFCAAL
                                                                                                         DĠVĀVĀQĪĠĀCNFEVCKDHVDEVĪTVGSDEĪCĀĀIKDIYDDTRSITEPĀĠĀLĀVĀĠIKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EHLVELGYRYKDETDNPAYRFFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERLYSFEFFEYPGALLKFLSMLGTHWNISLFNYRNHGADYGRVLCGFEL--DTPDLVRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDQLANIFVGVRLVGGPDELKSIIHELRQSGYPVQDLSDDEMAKLHIRYMIGGRPSKPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLSGANTNFHGLRYVSERCELGEKREGLLAVTIPERKGAFFDFCQIIGNRAVTEFNYRYN
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              53.8%; Score 1415.5; DB 2; 54.4%; Pred. No. 2.2e-91; tive 95; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                509
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246 251

TFRLCQEYLDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKXIALHNIRGERL

TERLCKELLDEIITVDTDAVCGAVKDIFDDTRSITEPAGALALAGLKAYIAREGAENQTL

FADAKNACIFVGVRLSRGLEERKEILQMLNDGGYSVVDLSDDEMAKLHVRYMVGGRPSHP

AHILSGANVNFHGLRYVSERCELGEQREALLAVTIPEEKGSFLKFCQLLGGRSVTEFNYR

IAVTSGANMNFHRLRHVSERSELGEGNEGIFAVTIPEERGSFLKFVNILGNRNITEFNYR

YGDDEKAHIFYGLQ-AAGPQDLAVIGSRLDEAGLPNVDLTDDEIAKIHIRYMVGGRTDKV

ENERLVSFEFPERPGALARFLNHMQGGWNITLFHYRNHGADYGRILVGIDVPPHDAAAFD

484

424 430

LQERLYSFEFPESPGAXLRFLNTLGTYWNISLFHYRSHGTDYGRVLAAFEXGDHE-PDFE

TRLNELGYDCHDETNNPAFRFFLA 513

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A;ACCESSAUM. ZIETA
A;Kolatus: preliminary
A;Molecule type: DNA
A;Residues: 1-508 <PAR>
A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84359.1; PID:g7379791)
A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84359.1; PID:g7379791)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: ilvA; NMA1096
C;Superfamily: threon:
C;Keywords: ammonia-l:
F;56/Binding site: py:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Raj Nature 404, 502-506, 2000

Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis A;Reference number: A81775; MUID:20222556; PMID:10761919

A;Accession: E81875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             threonine ammonia-lyase (EC 4.3.1.19) NMA1096 [similarity] - Neisseria meningitidis C;Species: Neisseria meningitidis C;Dace: 05-May-2000 #sequence_revision 05-May-2000 #text_change 21-Jun-2002 C;Accession: E81875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: E81875
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                                GLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDE
                                                                                                                                                 NFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHLD---RVFVPVGGG
                                                                                                                    SYNDAYDYAMELAEQEGLTYIAPFDDPDVIAGQGTVGMEIVSQ--HPDPIRAVFVPIGGG
                                                                                                                                                                                                                                                            TEEQKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRGFGGEVLLHGA
                                                                                                                                                                                                                                                                                                                                                                                                     AEYLRAVLRAPVYEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMAGL
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GLAAGVAAFIKOVRPEIKVIGVOTNDSCCMKOSVEAGEIVHLKDVGLFSDGTAVKVVGNE
                                                                                                                                                                                                                                  PKDALACGVIAASAGNHAQGVALSAQRLGCRAVIVMPETTPKIKVDAVKSRGGEVVLRGV
                                                                                                                                                                                                                                                                                                                                                SNYLIRILTASVYDVAVETPLEPARSLSVRLKNNILLKREDLOPVFSFKIRGAYNKMSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.6%; Score 1410.5; DB 2; 55.6%; Pred. No. 4.8e-91; tive 85; Mismatches 132;
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threonine ammonia-lyase (EC 4.3.1.19) NMBO878 [similarity] - Neisseria meningitidis (Str C;Species: Neisseria meningitidis (C;Species: Neisseria meningitidis (C;Species: Neisseria meningitidis (Str C;Species: Neisseria meningitidis (Str N. E.; Eisen, J.A; Neisseria meningitidis (Str N. E.; Eisen, J.A; Neisseria meningitidis (Str N. E.; Eisen, J.A; Neisseria (Str N. E.; Eisen, J., Str N. E.; Eisen, J.A; Neisseria (Str N. E.; Eisen, J., Str N. E.; Eisen, J.A; Neisseria (Str N. E.; Eisen, J., Str N. E.; Eisen, J., Neisseria (Str N. E.; Eisen, J., Neisseria (Str N. E.; Eisen, J.,
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E75502
threonine ammonia-lyase (EC 4.3.1.19) DR0567 [similarity] - Deinococcus radiodurans C;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jun-2002
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                                                                                                                                                                                                                                                         TRINELGYDCHDETNNPAFRFFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAVTSGAMMNFHRLRHVSERSELGEGNEGIFAVTIPEERGSFLKFVNILGNRNITEFNYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:AE002098; NID:g7226112; PIDN:AAF41289.1; PID:g722611
B, strain MC58
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                                                                      RESULT 12
F83603
           .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                  threonine dehydratase, biosynthetic PA0331 [imported] - C;Species: Pseudomonas aeruginosa
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; U S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium D A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: E75502 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-568 «MII»
A; Cross-references: GB: AE001915;
A; Experimental source: strain R1
C; Genetics:
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C;Superfamily: threonine dehydratase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase;
F;116/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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A;Gene: DR0567
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Matches 276; Conserv
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                                                                                                                                                TEFNYRFADAKNACIFVGVRLSRGLEERKEILQMLNDGGYSVVDLSDDEMAKLHVRYMVG
                                                                                                                                                                                          AEVILHGDSFSDAETFALALQQERGLTFVHPYDDPLVLAGQGTIALELLRQVEEDDYAVF
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                          EPD-----FETRLNELGYDCHDETNNPAFRFFL
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                                                                 GRAPEAVNERVYAFTFPERPGALHDFLTQLQGEWNISLFHYRNHGSAHGRVLAGVQV---
                                                                                     GRPSHPLQERLYSFEFPESPGAXLRFLNTLGTYWNISLFHYRSHGTDYGRVLAAFEXGDH
                                                                                                                               TEFNYRYAPREDAR I FVGVQLGQP-GERQELLTLLRGRGYAVLDLTEDELAKVHVRHMVG
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-PDAALTREGDELAGLGYPAHDVTSNPAYRLEL
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pred. No. 7e-89;
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T.; Zalewski,
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Coulter, A.L.,

Mizoguchi, S.D. r, S.N.; Folger,

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15-Sep-2000

#text_change S.D.; Warrener, lger, K.R.; Kas,

03-Jun-2002

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Hickey, Larbig,

M.J.; K.; Li

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Pseudomonas

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RESULT 13
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A12334

threenine ammonia-lyase (EC 4.3.1.19) [similarity] - Nostoc sp. (strain C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-C;Accession: A12334

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watar Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasu Nakazawa, M.; Yasu
                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-503 <KUR>
A;Cross references: GB:BF
A;Experimental source: sEC;Genetics:
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A;Gene: alr4232
C;Superfamily: threonine dehydratase
C;Keywords: ammonia-lyase; carbon-ni
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A;Status: preliminary
A;Molecule: type: DNA
A;Residues: 1-504 <5TO>
A;Cross-references: GB:AE004471;
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C;Superfamily: threon
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                                                                                                         GB:BA000019; PIDN:BAB75931.1; ce: strain PCC 7120
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%; Pred. No. 4.3e-87;
95; Mismatches 140;
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                                                                                                                                   PID:g17133367;
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09-Dec-2002
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Yasuda, M.; Tabata, S
                                                                                                                                                                                                                                                                                                    Cyanobacterium
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                                                                                                                                                                                                                                                                   LSGANVNFHGLRYVSERCELGEQREALLAVTIPEEKGSFLKFCQLLGGRSVTEFNYRFAD 373
                                                                                                                  RLYSFEFFESPGAXLRFLNTLGTYWNISLFHYRSHGTDYGRVLAAFEXGDHE-PDFETRL 492
                                                                                                                                                                                AKNACI FVGVRLSRGLEERKEILQMLNDGGYSVVDLSDDEMAKLHVRYMVGGRPSHPLQE
                                                                                                                                                                                                                                                                                                                          LCQEYVDEIILVDTDDTCAAIKDVFEDTRSILEPAGALAIAGAKAYVEREQIQGQTLVAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDLLAQGVIAASAGNHAQGVALGAKQLGTRAIIVMPVTTPQVKVDAVKARGGEVVLHGDT 123
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DSLGYQYWDESQNPAYKLFL
                                    NELGYDCHDETNNPAFRFFL 512
                                                                              LLYRFEFPERPGALMKFVASMSPNWNISMFHYRNNGSDYGRIVVGMQVPPQEMEEWQAFL
                                                                                                                                                               EKIAHIFIGMQI-QNRADKIHMVETFAECGFEILDLTDDELTKLHLRHMVGGHSPLAHNE
                                                                                                                                                                                                                                              ACGANMNFDRLRFVAERAEFGERREAIFAVTIPETPGSLRKFCECIGRRNLTEFNYRIAD
                                                                                                                                                                                                                                                                                                                                                                                                           SGIAAYVKRLRPEIKIIGVEPVDADAMNQSLQAGKRVRLSQVGLFADGVAVREVGEETFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDEAKAKAIELSQQQGFTWVPPFPHPMVIAGQGTLALELLQQ-DAHLDRVFVPVGGGGLA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYLRAVLRAPVYEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMAGLT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 106; Mismatches
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502
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C; Pariety: PCC 6803
C; Date: 25-Apr-10^C; Access: C;Accession: S77559
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis RESULT S77559 A;Cross-references: EMBL:D90905; GB:AB001339; A;Note: the nucleotide sequence was submitted threonine ammonia-lyase (EC 4.3.1.19) - Synechocystis sp. N;Alternate names: L-threonine deaminase; protein slr2072 A;Status: nucleic acid sequence A;Reference number: S74322; MUID:97061201; PMID:8905231 A;Accession: S77559 A; Molecule type: DNA ;Residues: 1-508 <KAN> not shown; translation NID:g1652360; PIDN:BAA17406.1; to the EMBL Data Library, June not (strain shown 20d PID:g165248 1996

á Matches Query Match Best Local 256; Similarity Conservative 49.6%; Pred. No. 9.9e-84; 96; Mismatches 145; Score 1306; DB 2; Pred. No. 9.9e-84; DB 2; Length 508; Indels 8 Gaps

;Superfamily: threonine dehydratase;Reywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase;;S1/Binding site: pyridoxal phosphate (Lys) (covalent) #status predict;

predicted

hydro-Lyase;

C;Genetics: A;Gene: ilvA

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A;Cross-references: EMBL:X01466; NID:g3821; PIDN:(C;Genetics:
A;Gene: SGD:ILV1; MIPS:YER086W
A;Cross-references: SGD:S0000888; MIPS:YER086W
A;Cross-references: SGD:S0000888; MIPS:YER086W
A;Genome: nuclear
C;Function:
A;Description: catalyzes conversion of threonine
A;Pathway: isoleucine biosynthesis
A;Note: first step
C;Superfamily: threonine dehydratase
C;Keywords: ammonia-lysse; carbon-nitrogen lysse;
F;109/Binding site: pyridoxal phosphate (Lys) (cc
                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9747, 8198, 9781, and 1 A;Reference number: S50436
A;Recession: S50589
A;Molecule type: DNA
A;Residues: 1-576 <DIE>
A;Cross-references: EMBL:U18839; NID:g603313; PIDN:AAB64641.1; PID:g603324; A;Cross-references: EMBL:U18839; NID:g603313; PIDN:AAB64641.1; PID:g603324; A;Cross-references: EMBL:U18839; NID:g603313; PIDN:AAB64641.1; PID:g603324; A;Cross-references: EMBL:U18839; NID:g603313; PIDN:AAB64641.1; PID:g603324; A;Cross-references: Commun. 49, 567-575, 1984
A;Title: Nucleotide sequence of the gene for threonine deaminase (ILV1) of S:A;Reference number: A01150
A;Molecule type: DNA
A;Residues: 1-258, T', 280-576 <KIE>
A;Residues: 1-258, T', 280-576 <KIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 threonine ammonia-lyase (EC 4.3.1.19) precursor - yeast N;Alternate names: protein YER086w; threonine deaminase C;Species: Saccharomyces cerevisiae C;Date: 17-May-1995 #sequence_revision 12-May-1995 #text C;Accession: S50589; A01150 R;Dietrich, F.S.
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                                      Superfamily: threonine dehydratase; Keywords: ammonia-lyase; carbon-oxygen lyase; homotetramer; 109/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                             Description: catalyzes conversion of threonine Pathway: isoleucine biosynthesis Note: first step
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Cross-references: EMBL:X01466; NID:g3821; PIDN:CAA25696.1; PID:g3823
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Search completed: December 18, Job time : 22 secs 2003, 15:30:14

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Result
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR TILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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US-09-252-991A-27783
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Best Local S
Matches 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27783, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: UNSURE
LOCATION: (108)
OTHER INFORMATION: Identity of amino
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                                                    GSEÄHIFVGVQTHPENDPREALVAYLREKGFPVLDLTDNELÄKLHIRHMVGGHAVKVSDE
                                                                      AKNACIFVGVRLSRGLEERKEILQMLNDGGYSVVDLSDDEMAKLHVRYMVGGRPSHPLQE
                                                                                                                    DSGANVNFDRLRHVAERAELGERREAIIAVTIPERPGSFKAFCEAVGKRQITEFNYRYHS
                                                                                                                                         LSGANVNFHGLRYVSERCELGEQREALLAVTIPEEKGSFLKFCQLLGGRSVTEFNYRFAD
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Pred. No. 5.3e-125;
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 ; Sequence 10, Application U
; Patent No. 5643779
; GENERAL INFORMATION:
APPLICANT: Ehrlich, St
; APPLICANT: Godon, Jean
                                                                                  RESULT 4
US-08-403-866-10
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Sequence 7451, Application US/093283:
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID ANI
TITLE OF INVENTION: BAUMANNII FOR D:
FILE REFERENCE: GTC99-03PA
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US-09-328-352-7451
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7451
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TYPE: PRT
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Local Similarity 51.9%;
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PDGLIET-LEQISYPYAEITDNVGYKRFL
                                 PD--FETRLNELGYDCHDETNNPAFRFFL
                                                                                                        SHPLOERLYSFEFFESFGAXLRFLNTLGTYWNISLFHYRSHGTDYGRVLAAFEXGD--HE
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Pred. No. 2.7e
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
                                                         Sequence 3876, Application US/09134001C Patent No. 6380370
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Best Local (
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TELEPHONE: (716) 263-1600
TELEPAX: (716) 263-1487
TELEX: 978450 (WUT)
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/403,86 FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                         IGDETFRICQEYLDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKYIALHNIR
                                                                                                                                                                                                                                                                                                                                                                                              IGGGGLIAGITAYSKERYPQTEIIGVEAKGATSMKAAYSAGQPVTLEHIDKFADGIAVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                 VGGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGDTFDESARAAKAFSQDNDKPFIDFFDDENVIAGQGTVALEIFAQAKKQGISLDKIFVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDEQRSKGVVCASAGNHAQGVAFAANQLNISATIFMPVTTPNQKISQVKFFGESHVTIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLSNKYQANIYLKEVVTKTPLQLDPYLSNKYQANIYLKEENLQKVRSFKLRGAYYSISKL
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; Pred. No. 3.2e-52;
74; Mismatches 151
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3876
LENGTH: 424
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application Patent No. 6107063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                     APPLICANT: Moeckel,
APPLICANT: Eggeling,
APPLICANT: Salm, Her
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
COMPUTER: IBM COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                     COUNTRY:
                                                                                                                                                     CITY: Washington
                                                                                                                                                                                         ADDRESSEE:
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                                                                                                       20007-5109
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Sahm, Hermann
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g, Lothar
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DEHYDRATASE
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                                                                                                                                                                                                                                                         PRODUCTION OF L-ISOLEUCINE RECOMBINANT MICROORGANISMS
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                   #1.0,
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                                                                                                                                                                                                                                                                   RESULT 7
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                                                                                                                                                                                                         Sequence 2, Application US/08669378 Patent No. 6107063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 145;
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Best Local Similarity
                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                      APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Hermann
TITLE OF INVENTION: PRODUCTION OF L-ISOLEUCINE
TITLE OF INVENTION: RECOMBINANT MICROORGANISMS
TITLE OF INVENTION: DEHYDRATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 09-JAN-
                                   CORRESPONDENCE ADDRESS:
                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                   APPLICANT: Moeckel, Bettina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 20-MAR CLASSIFICATION: 435
                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 HVMVPVGGGGLLAGVVSYMADMAPRTAIVGIEPAGAASMQAALHNGGPITLETVDPFVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 -- VILHGANFDEAKAKAIELSQQQGFTWVEPFDHPMVIAGQGTLALELLQQDAHL----D 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 RVFVPVGGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 GAEYLRA----VLRAPVYEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSLVVTGNNFDEASAAAHEDAERTGATLIEPFDARNTVIGQGTVAAEILSQLTSMGKSAD
                                                                                                                                                                                                                                                                                                                                                           -LLG-GRSVTEFNY-RFADAKNACIFVGVRLSR--GLE---ERKE
                                                                                                                                                                                                                                                                                                                                                                                                                                   IALHNIRGERLAHILSGANVNFHGLRY--VSERCELGEQREALLAVTIPEEKGSFLKFCQ
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(202)672-5399
3: Foley & Lardner
3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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20-MAR-1997
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 436 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: 904136
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FILING DATE: 14-JAN-1994
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TELEFAX: (202)672-5399
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                                                                                                                                                                                                                                                                                                                          137 VSLVVTGNNFDEASAAAHEDAERTGATLIEPFDARNTVIGQGTVAAEILSQLTSMGKSAD
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DILGPODDITLFEYLKRNNRETGTALVGIHLSEASGLDSLLERME
                                   -LLG-GRSVTEFNY-RFADAKNACIFVGVRLSR--GLE---ERKE 394
                                                                              --MSFAPGSAVVCIISGGNNDV--LRYAEIAERSLVHRGLKHYFLVNFPQKPGQLRHFLE
                                                                                                                                                            AEVKRVGDLNYTIVEKNQGRVHMMSATEGAVCTEMLDLYQNEGIIAEPAGALSIAGLKE-
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nilarity 35.6%;
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RESULT 8 US-09-328-352-5207 ; Sequence 5207, Application US/09328352 ; Patent No. 6562958 GENERAL INFORMATION:

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RESULT 9
US-08-669-378-10
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; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5207
                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6107063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10,
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5207
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Best Local :
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                           APPLICANT: Eggeling,
APPLICANT: Sahm, Her
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COPPRAFING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,378
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                               STREET: 3000 K St
CITY: Washington
                                                                                                                                                              COUNTRY: USA
FILING DATE:
                                                                                                                                                                                                                                        ADDRESSEE:
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 20-MAR-1997
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                                                                                                                                                                                                                                                                                               DEHYDRATASE
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                                                                                                                                                                                                                       Suite
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US-08-669-378-12

Sequence 12, Application Patent No. 6107063

US/08669378

Patent No.

GENERAL INFORMATION:

APPLICANT: Moeckel, Bett APPLICANT: Eggeling, Lot APPLICANT: Eggeling, Lot APPLICANT: Sahm, Hermann TITLE OF INVENTION: PROI TITLE OF INVENTION: DEHY NUMBER OF SEQUENCES: 18 CORRESSPONDENCE ADDRESS:

PRODUCTION OF L-ISOLEUCINE RECOMBINANT MICROORGANISMS DEHYDRATASE

WITH DERE

DEREGULATED THREONINE

Eggeling, Lot! Sahm, Hermann Moeckel, Bettina

Lothar

STREET: 3000 CITY: Washington

Suite 500

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RESULT 10
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APPLICATION NUMBER: DE P 4
FILING DATE: 14-7AN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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FILING DATE: 09-JAN-1995
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                                                                                                                                                             300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                              --VLLHGANFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHL----D
                                                                                                                                                                                                                                                                                                                                                                                                              SGAQSPQEQRDAGIVAASAGNHAQGVAYVCKSLGVQGRIYVPVQTPKQKRDRIMVHGGEF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAELIKAADIQTAQARISSVIAPTPLOYCPRLSEETGAEIYLKREDLODVRSYKIRGALN
                                                                                      -LLG-GRSVTEFNY-RFADAKNACIFVGVRLSR--GLE---ERKE 394
                                                                                                                         --MSFAPGSVVVCIISGGNNDV--LRYAEIAERSLVHRGLKHYFLVNFPQKPGQLRHFLE 371
                                                     DILGPODDITLFEYLKRNNRETGTALVGIHLSEASGLDSLLERME
                                                                                                                                                            IALHNIRGERLAHILSGANVNFHGLRY--VSERCELGEQREALLAVTIPEEKGSFLKFCQ 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 amino acids
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Pred. No. 5.8e-46;
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-669-378-12
                                                                                                  RESULT 11
US-08-669-378-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 144
Sequence 8, Application US/08669378
Patent No. 6107063
GENERAL INFORMATION:
APPLICANT: Moeckel, Bettina
APPLICANT: Eggeling, Lothar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 436 amino acid
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PRIOR APPLICATION DATA:
APPLICATION UMBER: DE P
APPLICATION UMBER: DE P
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29.76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
TELEPAX: 0223672-5399
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 20-MAI CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 5.8e-46;
3; Mismatches 160
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 0
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Beatt, Stephen A.
REGISTRATION NUMBER: 29,768
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APPLICATION NUMBER: US/
FILING DATE: 20-MAR-199
CLASSIFICATION: 435
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TITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: 1
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                 358
                                                     316 --MSFAPGSVVVCIISGGNNDV--LRYAEIAERSLVHRGLKHYFLVNFPQKPGQLRHFLE
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amino acid
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             -LLG-GRSVTEFNY-RFADAKNACIFVGVRLSR--GLE---ERKE 394
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                                                                                                                                                                                                                                                                                                                                                           SGAQSPQEQRDAGIVAASAGNHAQGVAYVCKSLGVQGRIYVPVQTPKQKRDRIMVHGGEF
                                                                                        IALHNIRGERLAHILSGANVNFHGLRY--VSERCELGEQREALLAVTIPEEKGSFLKFCQ
                                                                                                                                GEVKRVGDLNYTIVEKNQGRVHMMSATEGAVCTEMLDLYQNEGITÄEPAGALSIAGLKE-
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3000 K Street, N.W., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.7%; Score 546; DB 3; ilarity 35.6%; Pred. No. 1.1e-45; Conservative 73; Mismatches 160
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US-08-669-378-6
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; MOLECULE TYPE:
US-08-669-378-6
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Best Local Similarity
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APPLICATION NUMBER: DE P 44 00

FILLING DATE: 14-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29 768

REGISTRATION NUMBER: 29 768
                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: 20007-5109
COMPUTER READABLE FORM:
COMPUTER READABLE FLORDY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3000 K St
CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                  143;
                                                                    137 VSLVVTGNNFDEASAAAHEDAERTGATLIEPFDARNTVIGQGTVAAEILSQLTSMGKSAD
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 HVMVPVGGGGLLAGVVSYMADMAPRTAIVGIEPAGAASMQAALHNGGPITLETVDPFVDG
                           RVFVPVGGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEG 241
                                                                                                   ---VLLHGANFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHL----D
                                                                                                                                                                          MMAGLTEEQKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRGFGGE-
                                                                                                                                         SGAQSPQEQRDAGI VAASAGNHAQGVAYVCKSLGVQGRIYVPVQTPKQKRDRIMVHGGEF
                                                                                                                                                                                                             GAELIRAADIQTAQARISSVIAPTPLQYCPRLSEETGAEIYLKREDLQDVRSYKIRGALN 76
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                                                                                                                                                                                                                                                                                                                                                                                                                            436 amino acids
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Sahm, Hermann
                                                                                                                                                                                                                                                                                     Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE P 44 00
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                                                                                                                                                                                                                                                                              Score 541; DB 3; Length 43
Pred. No. 3.6e-45;
3; Mismatches 161; Indels
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SEQ ID NO 31294
LENGTH: 374
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                      356
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                                                                                                                                                                                                             236 GLFAEGVAVKRIGDETFRLCQEYLDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAG 295
                                                                                                                                                                                                                                                                                                                                           162 VKIEATRGYGGQVVLYDRYTEDREQIGRDLAQRHGLTLIPPYDHPDVLAGQGTAAKELFE 221
                                                                                                                                                                                                                                                                                                                                                                                                                               102 ORMGAFKFRGAFNALSRFSAEORAAGVVAFSSGNHAQATALSARLLGIPATIVMPADAPA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 VAVKRIGDETFRLCQEYLDDI--ITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119;
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CALLGG
                                      COLLIGG
                                                                                 ARQ--RKDELRGKRVGILLSGGNID-
                                                                                                                            MKKYIALHNIRGERLAHILSGANVNFHGLRYVSERCELGEQREALLAVTIPEEKGSFLKF 355
                                                                                                                                                                    QTLADGAQTQHLGNLTFPLIQRNVDDILTASDAELVDGMRFLAARMKLLVEPTGCLGLAA
                                                                                                                                                                                                                                                                                                QDAHLDRVFVPVGGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRV 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSGAPEGAEYLRAVLRAPVYE-----AAQV-----TPLQKMEKLSSRLDNVILVKREDR
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                                                                                                                                                                                                                                                        EVGPLDAFFAPLGGGGLLSGCALAIRALAPACRIYGVEPEAGNDGQRSLRSGAIVHIDTP 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEVKRVGDLNYTIVEKNOGRVHMMSATEGAVCTEMLDLYQNEGIIAEPAGALSIAGLKE-
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374
                                      361
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2e-42;
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RESULT 14 US-09-328-352-4536

Sequence 4536, Application US/09328352 Patent No. 6562958

GENERAL INFORMATION:

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; ORGANISM: Homo sapiens
US-09-789-300A-2
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US-09-789-300A-2
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4536
LENGTH: 328
TYPE: PRT
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Best Local Similarity
Matches 107; Conserv
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APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate
TITLE OF INVENTION: Dependent Enzyme Family Member and Uses Therefor
FILE REFERENCE: 35800/200926
FILE REFERENCE: 35800/200926
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 340
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                                                                                                                                                                    Query Match
Best Local Similarity
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CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: US 60/183,208
PRIOR FILING DATE: 2000-02-17
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308 IGIIISGGNVD 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 GGLAAGVAVLIKOLMPOIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGD 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 EFDRYTEDREKIGKEIAEKNGLTLIPSYDHPHVIAGOGTAAKELFEEVGDLDYLFVCLGG
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                                                 19
  82 VITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRGFGGEVLLHGANFDEAKAK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHGANFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHLDRVFVPVGG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLQFNETQKKAGVVAFSSGNHAQAIALSSKILGIPATIIMPKDAPAAKMAATREYGGNIV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAGLTEEQKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRGFGGEVL 129
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                                                 IRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKA 78
                                                                                           VYEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMAGLTE---EQKAHG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 449.5; DB 4; ilarity 34.4%; Pred. No. 2.9e-36; Conservative 58; Mismatches 133;
                                                                                                                                      .13.6%; Score 357; DB 4; Length 340; ilarity 30.7%; Pred. No. 4.8e-27; Conservative 66; Mismatches 134; Indels
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   318
                                  256 VDDIFTVTEDEIKCATOLVWERMKLLIEPTAGVGVAAVLSOHFOTVSPEVKNICIVLSGG
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                                                                                                                                 202 QLMPQIKVIAVE---AEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFRLCQEY 258
                                                                                                                                                                                                                                 79
                                                                                                  ALKPSVKVYAAEPSNADD---CYQSKLKGKLMPNLYPPETIADGVK-SSIGLNTWPIIRDL
                                                                LDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAG-MKKYIALHNIRGERLAHILSGA 317
                                                                                                                                                                                                                                 NVN 320
                                                                                                                                                                   AKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMLAGIAITVK 198
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Search completed: December 18, 2003, 15:30:48 Job time : 22 secs

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Result
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2: sp bacteria
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5: sp inverteb
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7: sp mhc:*
8: sp organel:
9: sp plane:*
10: sp plane:*
11: sp rodent:
12: sp vrius:*
13: sp vrius:*
14: sp unclass
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sp_rvirus:*
sp_bacteriap:*
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Q8X487
Q8X378
Q8Z378
Q8ZAB4
Q8ZAB4
Q8E9E0
Q9IV11
Q8E9E0
Q9IV11
Q9E9E0
Q9IXWI
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Q9ZWI
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Q9XYB7
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Q8z378
Q8ddab4
Q8de9e0
Q9iu11
Q8e9e0
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Q9ixVI
                                                                                                                                                                                                                                                                                                                                              Description
8 salmonella
4 yersinia pe
2 vibrio vuln
1 vibrio chol
1 shewanella
8 pseudomonas
5 neisseria m
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1 neisseria m
2 deinococcus
6 pseudomonas
7 raistonia s
7 synechocyst
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SI	ALIGNMENTS						
Q8en71 oceanobacil	Q8EN71	16	338	20.2	531	45	
112	Q8Z3K4	16	329	20.2	533	44	
	Q97CB2	17	406	20.6	543.5	43	
Q8fnw7 corynebacte	Q8FNW7	16	436	20.7	545.5	. 42	
	Q8YH69	16	419	20.9	551	41	
Q9rc71 bacillus ha	Q9RC71	N	370	21.0	554	40	
	TLAM6D	16	401	21.1	556	39	
Q9pp95 campylobact	Q9PP95	16	403	21.2	558.5	38	
Q9hnh6 halobacteri	Q9HNH6	17	495	21.5	566	37	
	Q9HLW2	17	406	21.7	570.5	36	
	Q92A24	16	422	21.9	577.5	35	
	Q8XL77	16	402	22.0	579.5	. 34	
	Q8DR02	16	416	22.0	580.5	33	
	Q97SD4	16	416	22.0	580.5	32	
Q8cnk9 staphylococ	Q8CNK9	16	424	22.2	583.5	31	
	Q8Y5R5	16	422	22.4	590.5	30	
	Q9EWG3	16	409	22.5	593	29	
	Q99SJ1	16	422	22.6	594	28	
Q8nvi8 staphylococ	Q8NVI8	16	422	22.7	597	. 27	
Q9xbi2 bacillus ce	Q9XBI2	N	420	22.8	601	26	
Q8g466 bifidobacte	Q8G466	16	415	22.9	603.5	25	
Q8rdt9 fusobacteri	Q8RDT9	16	404	23.2	610	24	
Q8dw42 streptococc	Q8DW42	16	416	23.3	612.5	23	
	Q9F7T0	N	404	33.4	880.5	22	
Q8gug5 arabidopsis	Q8GUG5	10	592	41.3	1088	. 21	
	Q9AXU4	10	601	41.6	1094.5	20	
Q9auq1 oryza sativ	Q9AUQ1	10	602	42.7	1123	19	
O94634 schizosacch	094634	ω	600	42.7	1123.5	18	
Q8w314 oryza sativ	Q8W314	10	602	44.8	1180.5	17	

Scoring table: Sequence: Title: Perfect score:

NP418220 2633

MADSQPLSGAPEGAEYLRAV.....LGYDCHDETNNPAFRFFLAG

514

Searched:

830525 seqs, Gapop 10.0 , BLOSUM62DX

258052604 residues

Gapext 0.5

Run

on:

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protein search, using sw model

Copyright

GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.

December 18, 2003, 15:27:16; Search time 39 Seconds (without alignments)

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RESULT 1 Q8X3IB ID Q8X3 AC Q8X3 AC Q8X3 AC O1-M DT 01-M DT 01-M DT 01-M C Inre GN ECS4 OS Esch OC Bact OC Rite OC NCBI RN [1] RN SEQU Q8X318 PRELIMINARY; Q8X318; Q8X318; 01-MAR-2002 (TrEMBLrel. 20, C 01-MAR-2002 (TrEMBLrel. 20, I 01-MAR-2003 (TrEMBLrel. 23, I Threonine deaminase. Escherichia coli 0157:H7. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia. SEQUENCE FROM N.A. NCBI_TaxID=83334; ECS4706. Created) Last sequence update) Last annotation update) 514 Ą

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Database

sp_archea:*
sp_bacteria:*

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Maximum Minimum

DB BB

seq

length:

2000000000

Total number of hits satisfying chosen parameters:

830525

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sp_rodent:*
sp_virus:*

sp_plant:*

sp_organelle:* sp_mammal:* sp_invertebrate:*

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Best Local Similarity 99.2%; Pred. No. 1.4e-174; Matches 510; Conservative 3; Mismatches 1;	99.6%; Score 2622; DB 16;	514 AA; 56184 MW; ACF4692F144FC8B5 CRC64;	Ħ,	TIGRFAMs; TIGR01124; ilvA_2Cterm; 1.			•			•			O157:H7 and genomic comparison with a laboratory strain K-12.";	"Complete genome sequence of enterohemorrhagic Escherichia coli	Kuhara S., Shiba T., Hattori M., Shinagawa H.;	Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,	Han CG., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,	Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,		
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Melch R.A., Burland V., Plunkett G. III, Redford P., Roesc Melch R.A., Burland V., Plunkett G. III, Redford P., Roesc D. Buckles E.L., Liou S.-R., Boutin A., Hackett J., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T. Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genon of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

REMBL; AE016769; AAN8126.1; -.

Lyase; Complete proteome.

Natly Medical Sci. U.S.A. 99:17020-17024(2002).

SEQUENCE 515 AA; 56285 MW; AF0F77C496585871 CRC64;
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Query Match 97.8%;
Best Local Similarity 98.1%;
Matches 505; Conservative
                                                                         EMBL; AE005608; AAG58967.1; -.

InterPro; IPR001226; B6 enzyme beta.

InterPro; IPR000634; S/T dehydrtse.

InterPro; IPR001721; ThrDh C.

InterPro; IPR005787; Thr_dehydrateI.

Pfam; PF00291; PALP; 1.

Pfam; PF00585; Thr_dehydrat C; 2.

TIGRPAM8; TIGR01124; ilvA_2Cterm; 1.

PROSITE; PS00165; DEHYDRATASE_SER_THR; 1
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01-MAR-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8X467;
Q8X467;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutain A., Shao Y., Miller L.,
Posfai G., Hackett J., Lim K., Dimalanta E.T., Potamousis K.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                      Escherichia coli 0157:H7.
Bacteria; Proteobacteria;
Enterobacteriaceae; Escher
NCBI_TaxID=83334;
                                                                                                                                                                                                  Nature
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                                                                                                                                                                                                 "Genome sequence of enterohaemorrhagic Nature 409:529-533(2001).
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Escherichia.
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A Parkhill J., Dougan G., James K.D., Holden M.T.G., Sebaihia M. A Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. A Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

A Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

A Cronin A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

A Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

A Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

T. Complete genome sequence of a multiple drug resistant Salmonella

T. Holder S., Barrell B.G.;

T. Word Control of the C
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Q8Z378;
Q8Z378;
Q1-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2002 (TrEMBLrel. 22,
Threonine deaminase.
STY3652.
Salmonella typhi.
Bacteria; Proteobacteria; G.
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
InterPro; IPR005787; Thr_dehydrateI.
Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 2.
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NCBI_TaxID=601;
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Query Match
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PROSITS; PS00165; DEHYDRATASE SER_THR;
Complete proteome.
SEQUENCE 514 AA; 56276 MW; 17B0E670
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94.9%;
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Pred. No. 1.9e
18; Mismatches
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SEQUENCE FROM N.A.

C STRAIN=CO-92 / Biowar Orientalis;

C STRAIN=CO-92 / Biowar Orientalis;

X MEDLINE=21470413; PubMed=11586360;

X MEDLINE=21470413; PubMed=11586360;

A Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

A Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

A Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.

A Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

A Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

A Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

A Feather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

A Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

T "Genome sequence of yersinia pestis, the causative agent of plague

L Nature 413:523-527(2001).
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Q8ZAB4;
01-MAR-2002
01-MAR-2002
01-MAR-2003
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Bacteria; Proteobacteria; Gam
Bacteria; Proteobacteria; Gam
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02 (TremBLrel. 20, Last sequence update)
03 (TremBLrel. 23, Last annotation update)
03 (TremBLrel. 23, Last annotation update)
dehydratase (EC 4.2.1.16) (Threonine deam
PO3896 OR Y0339.
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Matches 433
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Q8DDG;
Q8DDG;
01-MAR-2003 (TrEMBLrel.:
01-MAR-2003 (TrEMBLrel.:
01-MAR-2003 (TrEMBLrel.:
Threonine dehydratase.
VV11028.
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Pfam; PF00585; Thr debydrat C; 2.

TIGRFAMs; TIGR01124; ilvA_2Cterm; 1.

PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.

Lyase; Complete proteome

SEQUENCE 514 AA; 55935 MW; A49EA796A2
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InterPro; IPR000634; S/T dehydrtse.
InterPro; IPR001721; ThiDh C.
InterPro; IPR001787; Thr_dehydrateI.
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J. Bacteriol. 184:4601-4611(2002). 
EMBL; AJ414159; CAC93363.1; -. 
EMBL; AE013634; AAM83930.1; -.
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AA; 55935 MW; A49EA796A2CE6640
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Pred. No. 1.5e
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Q9KVW1;
Q9KVW1;
01-OCT-2000 (TrEMBLrel. 15
f 01-OCT-2000 (TrEMBLrel. 1:
T 01-OCT-2002 (TrEMBLrel. 2:
Threonine dehydratase.
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Best Local Similarity
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SEQUENCE
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Choy H.E.;
SEQUENCE FROM N.A.
STRAIN=El Tor N16961 / Serotype O1;
MEDLINE=20406833; PubMed=10952301;
                                                                                                                                     Threonine dehydr
VC0027.
Vibrio cholerae.
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Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                       NCBI_TaxID=666;
                                                                                                  Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
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70.78;
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                                                                                                                      Gammaproteobacteria;
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Pred. No. 2.1e
58; Mismatches
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annotation updat
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2.1e-123;
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367

372

491 427 432 307 312 247 252 187

Alteromonadales;

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RESULT
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AC Q8
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DT 01
DT 01
DT 01
DT T1
DT T1
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Best Local Similarity
Matches 354; Conserv
           Q8E9E0 PRELIMINARY;
Q8E9E0;
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
Threonine dehydratase.
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PROSITE; P
Complete p
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00291; PALP; 1.

Pfam; PF00585; Thr_dehydrat_C; 2.

TIGRPAMs; TIGR01124; ilvA_2Cterm; 1.

PROSITE; PS00165; DEHYDRATASE_SER_THR;
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InterPro; IPR000634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh C.
InterPro; IPR005787; Thr_dehydrateI.
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HSSP; P04968; 1TDJ.
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                                                                                                                                                                                                                                                                 ERLYSFEFPEYPGALLKFLSMLGTHWNISLFNYRNHGADYGRVLCGFEL--DTPDLVRFS
                                                                                                                                                                                                                                                                                ERLYSFEFPESPGAXLRFLNTLGTYWNISLFHYRSHGTDYGRVLAAFEXGDHEPD---FE
                                                                                                                                                                                                                                                                                                                                    DDQLANIFVGV
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Last sequence
Last anno
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Pred. No. 1.1e
34; Mismatches
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                                 sequence update) annotation update
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Shewanella oneidensis.
Bacteria; Proteobacteria; Gamm.
Alteromonadaceae; Shewanella.
NCBI TaxID=70863;
              Q9I418
Q9I418;
01-MAR-2001
01-MAR-2001
01-OCT-2002
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Wall Ler J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Felonome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";
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EMBL; AE015867; AAN57312.1; -.
TIGR; S04344; -.
Complete proteome.
SEQUENCE 545 AA; 58971 MW; 5CD1A
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C STRAIN=ATCC 15692 / PAO1;

X MEDILINE=20437337; PubMed=10984043;

X MEDILINE=20437337; PubMed=10984043;

X MEDILINE=20437337; PubMed=10984043;

A Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagron A Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan A Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. A Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A Smith K.A., Spencer D.H., Wong G.K.-S., Uz., Olson M.V.;

T "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

T opportunistic pathogen.";

R HSSP; P04968; 1TDJ.

R HSSP; P04968; 1TDJ.
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InterPro; IPR00634; 8/T dehydrtse.
InterPro; IPR001721; ThrDh_c.
InterPro; IPR005787; Thr_dehydrateI.
Pfam; PF00291; PALP; 1.
Pfam; PF00885; Thr_dehydrat_C; 2.
TIGRPAMB; TIGR01124; ilvA_2Cterm; 1.
PROSITE; P900165; DEHYDRATASE_SER_THR; 1.
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R InterPro; IPR001926; S/T_dehydrtse.

R InterPro; IPR001721; ThrDh_C.

R InterPro; IPR001721; ThrDh_C.

R InterPro; IPR005787; Thr_dehydrateI.

Pfam; PF00291; PALP; 1.

Pfam; PF00291; PALP; 1.

IIGRPAMs; TIGR01124; ilvA_2Cterm; 1.

PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.

Lyase; Complete proteome.
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MEDLINE=20222556; PubMed=10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Chu
Klee S.R., Morelli G., Basham D., Brown D., Chillingwo.

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin I
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.
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Whitehead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neiss
meningitidis Z2491.";
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EMBL; AL162755; CAB84359.1;
HSSP; P04968; 1TDJ.
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Bacteria; Proteobacteria; Betaproteobacteria;
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(TIEMBLrel. 15, Last sequence update)
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reonine dehydratase biosynthetic (EC 4
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AA; 55212 MW;
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Skelton
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Best Local Similarity
Matches 277; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JZW1;
01-OCT-2000
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Pfam; PF00585; Thr_dehydrat_C; 2.

TIGRPAMS; TIGR01124; ilvA_2Cterm; 1.

PROSITE; PS00165; DEHYDRATASE_SER_THR;
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InterPro; IPR000634; S/T dehydrtse.
InterPro; IPR001721; ThrDh C.
InterPro; IPR005787; Thr_dehydrateI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; NMB0878;
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MEDLINE=20175755; PubMed=10710307;
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                                                                                                                           GLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDE
                                                                                                                                                                                                                                                    NFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHLD---RVFVPVGGG
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TFRLCKELLDEIITVDTDAVCGAVKDIFDDTRSITEPAGALALAGLKAYIAREGAENQTL
                        TFRLCQEYLDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKYIALHNIRGERL
                                                                                                                                                                                                      SYNDAYDYAMELAEKEGLTYIAPFDDPDVIAGQGTVGMEIVSQ--HPDPIRAVFVPIGGG
                                                                                                                                                                                                                                                                                                          PKDALACGVIAASAGNHAQGVALSAQRLGCRAVIVMPETTPKIKVDAVKSHGGEVVLRGV
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Pred. No. 2.3e
89; Mismatches
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RESULT
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Best Local
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SEQUENCE
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InterPro; IPR001721; Thr dehydrate
Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat C; 2.
TIGRPAMS; TIGR01124; ilvA_2Cterm;
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White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
White O., Eisen J.A., Heidelberg J.F., Nelson W.C., Richardson D.L.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Mincon K.W., Pleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
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Threonine dehydratase, biosynthetic.
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01-OCT-2002
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  VPVGGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAV 244
                                                                                                  GEVILHGANFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHLD-RVF 184
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(TremBLrel. 13, Last sequence up
(TremBLrel. 22, Last annotation
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                                                                                                                              InterPro; IPR001926; B6 enzyme_beta.
InterPro; IPR001926; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
InterPro; IPR001721; Thr_dehydrateI.
Pfam; PF00291; PALP; 1.
Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 2.
TIGRPAMS; TIGR01124; 11vA_2Cterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Complete proteome.
SEGITENOTO
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Q916G0;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seque)
01-OCT-2002 (TrEMBLrel. 22, Last annot)
Threonine dehydratase, biosynthetic.
ILVAI OR PA0331.
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Complete
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STRAIN-ATCC 15692 / PAO1;

STRAIN-ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener Hickey M.J., Brinkman F.S.L., Hufinagle W.O., Kowalik D.J., Lagro Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                                                                                                                                                                                                                              opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa.
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EEQKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRGFGGEVLLHGAN
                                                EYLRAVLRAPVYEAAQVTPLQXMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMAGLT
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                                   QYVKKILTSRVYDVAVETPLQPARQLSERLGNQVLLKREDLQPVFSFKIRGAYNKVAQLT
                                                                                                                           504 AA;
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                                                                                                                           55351 MW; 055CEF43E5A18D73 CRC64;
                                                                                        51.4%;
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                                                                             95;
                                                                              Pred. No. 3.96
5; Mismatches
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( MEDLINE=21595285; PubMed=11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamot, A. Kanabae A., Iriguchi M., Ishikawa A., Kawashima K., A. Watanabe A., Iriguchi M., Ishikawa A., Matsunoto M., Matsuno A., Murakaki N., Shimpo S., Sugimoto M., Takazawa M., Yar Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yar Yasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence of the filamentous nitrog "Complete genomic sequence genomic sequence of the geno
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EMBL; APO03595; BAB75931.1; -.
InterPro; IPR001926; B6 enzyme beta.
InterPro; IPR001926; S/T dehydrtse.
InterPro; IPR001721; ThrDh C.
InterPro; IPR005787; Thr_dehydrateI.
Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 2.
TIGRPAMS; TIGR01124; ilva_2Cterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
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                           EMBL; AL646059; CAD13977.1; -.

InterPro; IPR001926; B6 enzyme beta.
InterPro; IPR001926; B7 dehydrtse.
InterPro; IPR001721; ThrDh_C.
InterPro; IPR001721; ThrDh_C.
InterPro; IPR005787; Thr_dehydrate1.
Pfam; PF00291; PALP; 1.
Pfam; PF00291; PALP; 1.

ITGREAMS; TIGR01124; 11vA 2Cterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Lyase; Complete proteome.
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Q8Y287;
                                                                                                                                                                                                                                                                                                                 Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; "Genome sequence of the plant pathogen Ralstonia solanacearum.";
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Probable threonine dehydratase (Threonine deaminase)
protein (EC 4.2.1.16)
ILVA OR RSC0449 OR RSC04453.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
      SEQUENCE
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